

$$\begin{array}{r} 1675 \\ 57 \\ \hline 1574 \end{array}$$

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Qy	241		GAAACCCATAACTTCATCGCTTGTGGTTATTCTTCTCGGCCTGTTACCTTCATGGACAAA	300
Db	291		GAAACCCATAACTTCATCGCTTGTGGTTATTCTTCTCGGCCTGTTACCTTCATGGACAAA	350
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ORGANISM Arabidopsis thaliana  
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1  
AUTHORS Kim,G.T., Tsukaya,H. and Uchimiya,H.  
TITLE The ROTUNDIFOLIA3 gene of Arabidopsis thaliana encodes a new member  
of the cytochrome P-450 family that is required for the regulated  
polar elongation of leaf cells  
JOURNAL Genes Dev. 12 (15), 2381-2391 (1998)  
PUBMED 9694802  
REFERENCE 2 (bases 1 to 1934)  
AUTHORS Kim,G., Tsukaya,H. and Uchimiya,H.  
TITLE Direct Submission  
JOURNAL Submitted (13-OCT-1997) Gyung-Tae Kim, Institute of Molecular and  
Cellular Biosciences, Laboratory of Cellular Function; Bunkyo-ku,  
Yayoi 1-1-1, Tokyo 113, Japan  
(E-mail:j30359@unix.cc.u-tokyo.ac.jp, Tel:+81-3-3812-2111,  
Fax:+81-3-3812-2910)  
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ORIGIN

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Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-507-106-4 (1-524) x AB008097 (1-1934)

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Db	111	AATTACATGGATTATTTGGTCGCTGGTTTCTTGGTTTGTACGGCCGGAATACTTCTCCGT	170
Qy	41	ProTrpLeuTrpPheArgLeuArgAsnSerLysThrLysAspGlyAspGluGluGluAsp	60
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Qy	81	GluThrLeuAsnPheIleAlaCysGlyTyrSerSerArgProValThrPheMetAspLys	100
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Qy	121	SerThrAspAlaGluValAsnLysValValLeuGlnAsnHisGlyAsnThrPheValPro	140
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Db	471	GCATACCCTAAATCAATTACGGAACACTTGGAGAAAACCTCTATTCTCAGCATCAATGGA	530
Qy	161	ProHisGlnLysArgLeuHisThrLeuIleGlyAlaPheLeuArgSerProHisLeuLys	180
Db	531	CCTCATCAAAAAAGGCTTCACACGCTCATTGGCGGTTCCCTCAGATCTCCTCACCTCAA	590
Qy	181	AspArgIleThrArgAspIleGluAlaSerValValLeuThrLeuAlaSerTrpAlaGln	200
Db	591	GACCGGATCACTCGAGACATTGAGGCCTCGGTTGTTCTCACTTTGGCGTCTTGGGCTCAA	650
Qy	201	LeuProLeuValHisValGlnAspGluIleLysLysMetThrPheGluIleLeuValLys	220
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Qy	221	ValLeuMetSerThrSerProGlyGluAspMetAsnIleLeuLysLeuGluPheGluGlu	240
Db	711	GTGTTGATGAGCACATCTCCTGGTGAAGATATGAACATTCTCAAACCTGAGTTCGAAGAA	770
Qy	241	PheIleLysGlyLeuIleCysIleProIleLysPheProGlyThrArgLeuTyrLysSer	260
Db	771	TTCATCAAAGGTTTGATTTGTATCCCAATCAAATTCCCTGGCACTAGACTCTACAAATCC	830
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Db	831	TTAAAGGCGAAAGAGAGGTTAATAAAGATGGTAAAAAGGTTGTGGAGGAGAGACAAGTG	890
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Qy	321	IleProGlyGluGluThrMetProThrAlaMetThrLeuAlaValLysPheLeuSerAsp	340
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Qy	501	MetLysArgArgLeuProIleArgValAlaThrValAspAspSerAlaSerProIleSer	520
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